

## SEQUENCE LISTING

<110> The Research Foundation for Microbial diseases of Osaka University

<120> Japanese Encephalitis

<130> P98AF308-2

<140>

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&lt;170&gt; PatentIn Ver. 2.0

**<210> 1**

**<211> 1500**

## <212> DNA

<213> Japanese encephalitis virus

**<220>**

**<221> CDS**

**<222> (1)..(1500)**

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gga gcc act tgg gtg gat ttg gtg tta gaa gga gat agt tgt ttg aca 96  
Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Leu Thr  
20 25 30

tc atg gca aac gac aaa cca aca cta gal gtc cgc atg atc aac att 144  
 le Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile  
 35 40 45

aa gct agc caa ctt gct gaa gtc agg agt tac tgc tat cac gct tca 192  
lu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser  
50 55 60

tc	act	gac	att	tca	acg	gtg	gct	cga	tgc	ccc	acg	act	gga	gaa	gcc	240
al	Thr	Asp	Ile	Ser	Thr	Val	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	
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ac aac gag aaa cgt gct gac agc agc tac gtg tgc aaa caa ggc ttt 288  
is Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe  
85 90 95

act gac cgc gga tgg gga aat gga tgt gga ctt ttc ggg aaa gga agc 336  
 Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser  
 100 105 110

att gac aca tgc gca aaa ttt tct tgt acc agt aag gcc att gga aga 384  
 Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser Lys Ala Ile Gly Arg  
 115 120 125

atg atc caa cca gag aac atc aag tac gag gtt ggc ata ttc gtg cac 432  
 Met Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His  
 130 135 140

ggg acc acc acc tcg gaa aac cat ggg aat tac tca gcg caa gta gga 480  
 Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly  
 145 150 155 160

gcg tct caa gca gca aag ttt act gta act cca aac gct ccc tca ata 528  
 Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile  
 165 170 175

acc ctc aag ctt ggt gat tat gga gag gtc aca ctg gat tgt gaa cca 576  
 Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro  
 180 185 190

agg agt gga ctg aac act gaa gcg ttc tat gtc atg acc gtg ggt tcg 624  
 Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser  
 195 200 205

aag tca ttc tta gtc cat agg gaa tgg ttc cat gac ctt tct ctt ccc 672  
 Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ser Leu Pro  
 210 215 220

tgg acg tcc cct tca agc acg gca tgg agg aac aga gaa ctc ctc atg 720  
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 225 230 235 240

gaa ttt gaa gag gca cat gcc aca aaa caa tct gtc gta gcc ctt ggg 768  
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 245 250 255

tca cag gag gga ggc ctc cat caa gcg ttg gca gga gcc atc gtg gtg 816  
 Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val  
 260 265 270

gag tac tcg agc tca gtc aag tta aca tca ggt cac ctg aaa tgc agg 864  
 Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
 275 280 285

002090"4025550

cta aaa atg gac aaa ctg gct ctg aag ggc acg act tat ggc atg tgt 912  
 Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr Thr Tyr Gly Met Cys  
 290 295 300

aca gaa aaa ttc tgc ttc gcg aaa aat cca gcg gac aca ggc cat gga 960  
 Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His Gly  
 305 310 315 320

aca gtt gtc att gag ctc aca tat tct gga agc gat ggc tcc tgt aaa 1008  
 Thr Val Val Ile Glu Leu Thr Tyr Ser Gly Ser Asp Gly Ser Cys Lys  
 325 330 335

att ccg att gtc tca gtt gcg agc ctc aat gac atg acc cct gtg ggg 1056  
 Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val Gly  
 340 345 350

agg ctg gta aca gta aac ccc ttc gtt gcg aca tct agc tcc aac tca 1104  
 Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ser Asn Ser  
 355 360 365

aag gtg ctg gtt gag atg gaa cct ccc ttc gga gac tct tat atc gtg 1152  
 Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 370 375 380

gtt gga aga ggg gac aag cag att aac cat cac tgg cac aaa gct gga 1200  
 Val Gly Arg Gly Asp Lys Gln Ile Asn His His Trp His Lys Ala Gly  
 385 390 395 400

agc acg ctg ggc aaa gcc ttc tca aca act ttg aaa ggg gct cag aga 1248  
 Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg  
 405 410 415

tta gca gcg cta ggt gac aca gcc tgg gac ttc ggc tcc att gga ggg 1296  
 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
 420 425 430

gta ttc aac tcc ata ggg aaa gct gtt cac caa gta ttt ggc ggt gca 1344  
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 435 440 445

ttc aga acg ctc ttt ggg gga atg tct tgg atc aca caa gga cta atg 1392  
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met  
 450 455 460

ggg gcc ttg ctt ctt tgg atg ggt gtc aac gca cga gac cgg tca atc 1440  
 Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile  
 465 470 475 480

002090-4025560

gcc ctg gct ttt ttg gcc acg gga ggt gtg ctc gtg ttt tta gcg acc 1488  
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 <213> Japanese encephalitis virus

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Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Leu Thr  
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Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile  
 35 40 45

Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser  
 50 55 60

Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala  
 65 70 75 80

His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe  
 85 90 95

Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser  
 100 105 110

Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser Lys Ala Ile Gly Arg  
 115 120 125

Met Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His  
 130 135 140

Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly  
 145 150 155 160

Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile  
 165 170 175

Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro  
180 185 190

Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser  
195 200 205

Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ser Leu Pro  
210 215 220

Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn Arg Glu Leu Leu Met  
225 230 235 240

Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser Val Val Ala Leu Gly  
245 250 255

Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val  
260 265 270

Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
275 280 285

Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr Thr Tyr Gly Met Cys  
290 295 300

Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His Gly  
305 310 315 320

Thr Val Val Ile Glu Leu Thr Tyr Ser Gly Ser Asp Gly Ser Cys Lys  
325 330 335

Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val Gly  
340 345 350

Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ser Asn Ser  
355 360 365

Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
370 375 380

Val Gly Arg Gly Asp Lys Gln Ile Asn His His Trp His Lys Ala Gly  
385 390 395 400

Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg  
405 410 415

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
420 425 430

002090-4025560

Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 435 440 445

Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met  
 450 455 460

Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile  
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Asn Val His Ala  
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<212> DNA

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<220>

<221> CDS

<222> (1).. (1500)

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gga gcc act tgg gtg gac ttg gtg cta gaa gga gac agc tgc ttg aca 96  
 Gly Ala Thr Trp Val Asp Leu Val Glu Gly Asp Ser Cys Leu Thr  
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atc atg gca aac gac aaa cca aca ttg gac gtc cgc atg atc aac atc 144  
 Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile  
 35 40 45

gaa gct agc caa ctt gct gag gtc aga agt tac tgc tat cat gct tca 192  
 Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser  
 50 55 60

gtc act gac atc tcg acg gtg gct cgg tgc ccc acg act gga gaa gcc 240  
 Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala  
 65 70 75 80

cac aac gag aag cga gct gat agt agc tat gtg tgc aaa caa ggc ttc 288  
 His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe  
 85 90 95

act gal cgt ggg tgg ggc aac gga tgt gga ctt ttc ggg aag gga agt	336
Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser	
100 105 110	
att gac aca tgt gca aaa ttc tcc tgc acc agg aaa gcg att ggg aga	384
Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Arg Lys Ala Ile Gly Arg	
115 120 125	
aca atc cag cca gaa aac atc aaa tac gaa gtt ggc att ttt gtg cat	432
Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His	
130 135 140	
gga acc acc act tcg gaa aac cat ggg aat tat tca gcg caa gtt ggg	480
Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly	
145 150 155 160	
gcg tcc cag gcg gca aag ttt aca gta aca cct aat gct cct tcg ata	528
Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile	
165 170 175	
acc ctc aaa ctt ggt gac tac gga gaa gtc aca ctg gac tgt gag cca	576
Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro	
180 185 190	
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Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser	
195 200 205	
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Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ala Leu Pro	
210 215 220	
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Trp Thr Pro Pro Ser Ser Thr Ala Trp Arg Asn Arg Glu Leu Leu Met	
225 230 235 240	
gaa ttt gaa gag gcg cac gcc aca aaa cag tcc gtt gtt gct ctt ggg	768
Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser Val Val Ala Leu Gly	
245 250 255	
tca cag gaa gga ggc ctc cat cag gcg ttg gca gga gcc atc gtg gig	816
Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val	
260 265 270	
gag tac tca agc tca gtg aag tta aca tca ggc cac cta aaa tgc agg	864
Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg	
275 280 285	

ctg aaa atg gac aaa ctg gct ctg aaa ggc aca acc tat ggt atg tgc 912  
 Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr Thr Tyr Gly Met Cys  
 290 295 300

aca gaa aaa ttc tgc ttc gcg aaa aat ccg gcg gac act ggt cac gga 960  
 Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His Gly  
 305 310 315 320

aca gtt gtc att gaa ctt tca tac tct ggg agt gat ggc ccc tgc aag 1008  
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 325 330 335

att ccg att gtc tcc gtt gct agc ctc aat gac atg acc ccc gtc ggg 1056  
 Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val Gly  
 340 345 350

cgg ctg gtg aca gtg aac ccc ttc gtc gcg act tcc agc gcc aac tca 1104  
 Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ala Asn Ser  
 355 360 365

aag gtg ctg gtc gag atg gaa ccc ccc ttc gga gac tcc tac atc gta 1152  
 Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 370 375 380

gtt gga agg gga gac aag cag att aac cac cat tgg tac aag gct gga 1200  
 Val Gly Arg Gly Asp Lys Gln Ile Asn His His Trp Tyr Lys Ala Gly  
 385 390 395 400

agc acg ctg ggc aaa gcc ttt tca acg act ttg aag gga gct caa aga 1248  
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 405 410 415

ctg gca gcg ttg ggc gac aca gcc tgg gac ttt ggc tct att gga ggg 1296  
 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
 420 425 430

gtc ttc aac tcc ata ggg aaa gct gtt cac caa gtg ttt ggt ggt gcc 1344  
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 435 440 445

ttc aga aca ctc ttt ggg gga atg tct tgg atc aca caa ggg cta atg 1392  
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met  
 450 455 460

ggg gcc cta cta ctt tgg atg ggc atc aac gca cga gac cga tca att 1440  
 Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile  
 465 470 475 480



gcl ttg gcc ttc tta gcc aca gga ggl glg ctc glg ttc tta gcl acc 1488  
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 Asn Val His Ala 1500  
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<210> 4  
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 <212> PRT  
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                     20                    25                    30

Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile  
                     35                    40                    45

Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser  
                     50                    55                    60

Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala  
   65                    70                    75                    80

His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe  
                     85                    90                    95

Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser  
                     100                    105                    110

Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Arg Lys Ala Ile Gly Arg  
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Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His  
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Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly  
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Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile  
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Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro  
180 185 190

Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser  
195 200 205

Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ala Leu Pro  
210 215 220

Trp Thr Pro Pro Ser Ser Thr Ala Trp Arg Asn Arg Glu Leu Leu Met  
225 230 235 240

Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser Val Val Ala Leu Gly  
245 250 255

Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val  
260 265 270

Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
275 280 285

Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr Thr Tyr Gly Met Cys  
290 295 300

Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His Gly  
305 310 315 320

Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser Asp Gly Pro Cys Lys  
325 330 335

Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val Gly  
340 345 350

Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ala Asn Ser  
355 360 365

Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
370 375 380

Val Gly Arg Gly Asp Lys Gln Ile Asn His His Trp Tyr Lys Ala Gly  
385 390 395 400

Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg  
405 410 415

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
420 425 430

Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 435 440 445

Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met  
 450 455 460

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile  
 465 470 475 480

Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr  
 485 490 495

Asn Val His Ala  
 500

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